Chitinases CtcB and CfcI modify the cell wall in sporulating aerial mycelium of Aspergillus niger

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Table S1. Primers used in this study

Name	Target	Sequence	Underlined feature
F60	dTomato	GCATCCCATGGTGAGCAAGGGCGAGG	*Nco*I
R60	dTomato	GTCACGAATCTTGTACAGCTCGTCCATGC	*Bsr*GI
F61	P*cfcI*	ATCGAGCGGCCGCATGGGACCCTGCGCG	*Not*I
R61	P*cfcI*	ATAGCCATGGTTTGCTAATACTTGTTGATTAAGACCTTGG	*Nco*I
F68	*pyrG*	CTACACATGTCTCGGTCGCTCACTGTTC	*Pci*I
R68	*pyrG*	GTACACATGTCCGACGGAGTAGCCGAGAG	*Pci*I
F66	P*ctcB*	CCATGGAGTGTAAGGAAGGAATAAAGAG	*Nco*I
R66	P*ctcB*	GCGGCCGCGGTTCTAGTTGTCGGTC	*Not*I
F37	*cfcI* 1 kbp upstr.	GGGGACAACTTTGTATAGAAAAGTTGCTCCTTTGACTATGGGAGTG	*att*B4
R37	*cfcI* 1 kbp upstr.	GGGGACTGCTTTTTTGTACAAACTTGATCTGTGTTGTCCCACCTG	*att*B1r
F32	*cfcI* 1 kbp downstr.	GGGGACAGCTTTCTTGTACAAAGTGGTGAAGTCTTTCCTTATTAAAGAGTTTG	*att*B2r
R32	*cfcI* 1 kbp downstr.	GGGGACAACTTTGTATAATAAAGTTGAGCTCCCAAGACTCCGACGGC	*att*B3
F15	*cfcI*	GATAAGTCGAATTCATGAGCCTGCAGTGCGTGGC	
R15	*cfcI*	GGGTGACCAAGCTTTCAATGATGATGATGATGATGTGTCTGCGGTATCCCACG	
F44	*cfcI* 1.5 kbp upstr.	GCTCAGTCCGATCCTCAAGTC	
R38	*pyrG*	ATGATGTGGGCCCACTCAG	
F48	*ctcB* 1 kbp upstr.	GGGGACAACTTTGTATAGAAAAGTTGGACGGTCAGGAGATAATGG	*att*B4
R48	*ctcB* 1 kbp upstr.	GGGGACTGCTTTTTTGTACAAACTTGGTGTAAGGAAGGAATAAAGAG	*att*B1r
F49	*ctcB* 1 kbp downstr.	GGGGACAGCTTTCTTGTACAAAGTGGTTTGTGATACCCCTTGTAG	*att*B2r
R49	*ctcB* 1 kbp downstr.	GGGGACAACTTTGTATAATAAAGTTGTCCCACGACAATCACATC	*att*B3
F27	*ctcB*	GATCGACATATGAAGCTCGACTTGTCTTCCTCTAAC	
R27	*ctcB*	GAGATCGGATCCTCATTTCTTCCAGTTAGTGC	
F52	*ctcB* 1.5 kbp upstr	ACGGTCACCTCCCACCAATG	
R54	*HpH*	GCCTCCAGAAGAAGATGTTG	
BN016	*PnagA*	ATAAGAATGCGGCCGCTTTCGCGCCAGTCATGTGAC	*Not*I
BN017	*PnagA*	CATGCCATGGGGTAAAAGTGGAAACAGGGTACAATTAG	*Nco*I

attBIHygBf	*HpH* cassette	GGGGACAAGTTTGTACAAAAAAGCAGGCTAGGATTTCGGCACGGCTAC	*att*B1
BN104	*HpH* cassette	GGGGACCACTTTGTACAAGAAAGCTGGGTTGTGGAGTGGGCGCTTACAC	*att*B2

Table S2A. Transcription in dormant and germinating spores of genes that were induced in vegetative mycelium †.

ORF	Name	0 h	2 h	4 h	6 h	8 h
An01g11660	CbhB	12	15	13	14	15
An07g08640	AgnB	20	21	18	17	14
An11g03340	AamA	12	12	12	12	12
An08g10780	GbgA	12	12	12	12	12
An12g05010	AceA	12	12	12	12	12
An01g11670		15	12	12	12	12
An16g05970		21	12	12	12	80*
An07g08950	EglB	16	12	12	12	12
An03g04190		37	34	42	37	146*
An16g07040	BgtE	14	82*	481	1148	2037
An11g00200		27	12	12	12	14
An09g02160	RgaeA	12	12	12	12	12
An12g08280	InuE	27	44	36	41	33
An09g00670	GelD	12	14	12	12	12
An03g01050		46	14	18	17	15
An09g01190	AbnA	12	12	12	12	12
An03g06550	GlaA	30	12	12	15	20
An08g09610	AgnD	15	14	12	12	16
An07g09330	CbhA	13	13	12	12	13
An04g06920	AgdA	78	29*	29	36	36
An14g02670		33	17	20	30	24
An01g00780	XynB	17	12	22	79	86
An16g09040		470	12*	15	12	14
An07g08940		13	12	12	12	12
An16g06800		34	30	30	51	127
An09g06400	CtcA	32	35	170*	805	1321
An18g00730		18	14	15	29	145
An08g01760		28	14	12	12	12
An02g11150	AglB	19	17	18	16	12
An01g11010	CrhD	54	1256*	78	84	364
An01g01870	EglC	18	28	26	19	21
An05g01750		14	12	13	15	12
An07g01160	CrhC	12	108*	102	83	109
An02g12450	PgxC	13	12	12	12	15
An11g06080		16	17	17	13	12
An02g07020	CfcA	46	15*	12	20	76
An07g08710	TpsB	121	45	100	87	99
An14g01770		12	12	12	12	12
An06g00360	DfgF	31	48	107	125	135
An16g02760		12	12	12	12	12
An01g03340		35	27	21	26	26

† Gene expression in dormant (0 h) or germinating spores after indicated number of hours, displaying expression values and fold changes obtained from transcriptome analysis, with * significant (FDR q-value ≤ 0.05) fold change between indicated time point and previous time point.

Table S2B. Transcription in dormant and germinating spores of genes that were induced in aerial structures†.

ORF	Name	0 h	2 h	4 h	6 h	8 h
An15g07370		90	25	14	12	14
An14g05340	UrhgB	33	12	12	12	12
An03g02880		42	12*	12	12	12
An02g03980	KslA	13	12	12	12	12
An09g05920	CtcB	34	12	12	12	12
An04g09400		12	12	12	12	12
An02g13580	CfcI	109	16*	14	13	12
An06g01530	BgtD	35	33	30	23	19
An02g00850		43	27	16	20	15
An10g00400	GelA	36	716*	455	480	751
An09g02240	NagA	110	12*	12	12	12
An08g11070	SucA	13	12	12	12	12
An01g06500	DfgD	43	17	19	19	15
An15g03330		36	99	68	69	39
An18g01410	DfgA	18	18	12	12	12
An11g02090		47	12*	12	12	72*
An06g01140		14	22	23	23	28
An14g00660	ChsC	73	23*	19	52	69
An03g00740	DfgB	17	17	12	16	14
An01g09510		21	45	37	36	42
An01g14650	RgxA	15	13	12	12	12
An16g02850	CrhF	69	62	52	112	142
An01g04570		105	38	52	63	147
An03g05010		263	64	86	73	58
An02g13180	BgxB	63	14*	16	19	20
An02g09050	GelG	41	12	12	12	12
An02g02980		23	78*	62	98	129
An04g05940		41	59	65	68	96
An02g00610		12	126*	12	13	12
An04g04790		12	12	12	12	23
An01g09290		1203	17*	60	87	178
An16g02910		22	12	12	12	13
An09g06260	AgnC	187	12*	12	12	12
An15g01420		28	59	140	191	378
An16g08570	SttC	43	107	272	515	778
An11g02100		125	12*	13	12	12
An02g13520		37	12	12	12	22
An03g00500		25	20	14	18	21
An18g04100	ExgA	47	20	27	24	21
An09g06340		13	12	31	50	80
An02g03260	AgsD	16	22	14	13	12

† Gene expression in dormant (0 h) or germinating spores after indicated number of hours, displaying expression values and fold changes obtained from transcriptome analysis, with * significant (FDR q-value ≤ 0.05) fold change between indicated time point and previous time point.